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**Graphical abstract:** Whole genome screening of Guangxi Three-Yellow chicken reveals some distinctive genetic footprints of this indigenous breed of chicken in the Southern China. These data provide important information for improvement of fowl breeding and for studies on the phenotypic variation and the prevention or treatment of certain diseases of chicken.



Liao Y, Sun J, Huang Y, Wei F, Mo G, Zellmer L and Liao DJ (2020). Genomic Analysis Reveals Strong Signatures of Selection in Guangxi Three-Yellow Chicken in China. *J. World Poultry Res.*, 10 (3): 407-428. DOI: <https://dx.doi.org/10.36380/jwpr.2020.48>

## Research Paper

### Genomic Analysis Reveals Strong Signatures of Selection in Guangxi Three-Yellow Chicken in China.

Liao Y, Sun J, Huang Y, Wei F, Mo G, Zellmer L and Liao DJ.

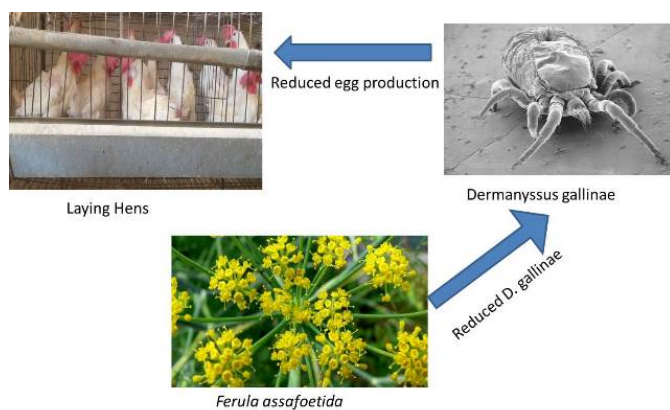
*J. World Poult. Res.* 10(3): 407-428, 2020; pii: S2322455X2000048-10

DOI: <https://dx.doi.org/10.36380/jwpr.2020.48>

**ABSTRACT:** Much like other indigenous domesticated animals, Guangxi Three-yellow chickens (GX-TYC) in China have experienced strong selective pressure, and show specific phenotypic changes in physiology, morphology and behavior. To identify genomic footprints or selection signatures left by artificial selection during domestication of GX-TYC, the whole genomes of 12 GX-TYC hens were sequenced to executed selective sweep analyses and gene functional enrichment analysis (Gene Ontology and Kyoto Encyclopedia of Genes and Genome pathways). A total of 10.13 million single nucleotide polymorphisms and 842,236 insertion/deletion polymorphisms (Indels) were found. Forty-six windows showed a Z score of heterozygosity (ZHp) lower than -5, which potentially were considered to be positively selected regions. Gene annotation identified 55 genes in these regions. Selection signatures were found mainly on the SSC5, SSC8, SSC23 and SSCZ. GO and KEGG analyses revealed that these genes were related to growth, immune responses as well as carbohydrate, lipid and amino acid metabolisms. In addition, two genes, fructose-1,6-bisphosphatase 1 and fructose-1,6-bisphosphatase 2 were enriched into four signaling pathways, three of which are involved in carbohydrate metabolism and insulin signaling. SHC3, FANCC and PTCH1, in combination with FB1 and FBP2, were clustered together in a region of chromosome Z, and thus might have been selected together. The results have uncovered some genetic footprints of chicken domestication, providing not only an important resource for further improvements of fowl breeding, but also a useful framework for future studies on the genetics of domestic chickens as well as on the phenotypic variations and certain diseases of chickens.

**Key words:** Chicken; Selective sweeps; Single nucleotide polymorphism; Whole genome resequencing

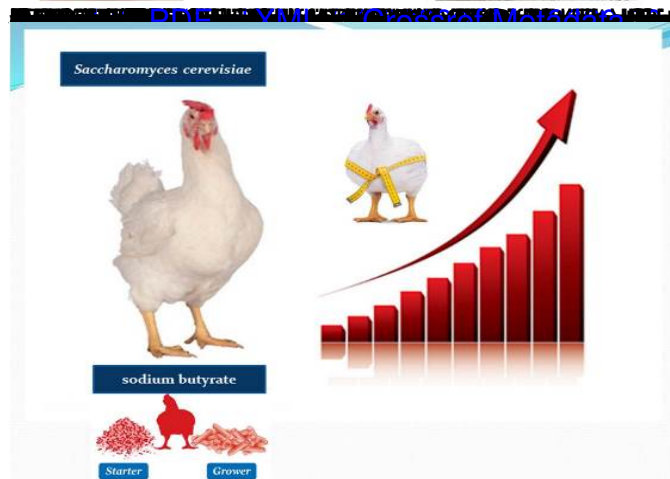
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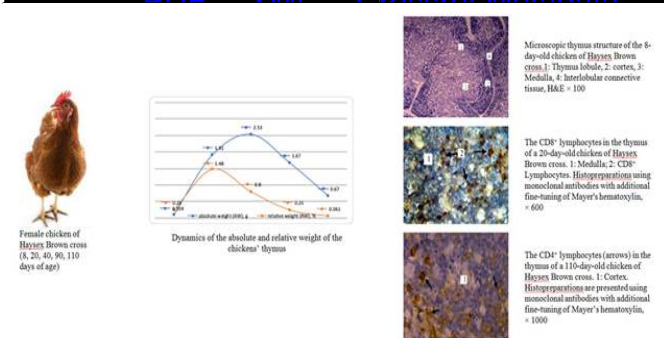
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### Production Performances of Indonesian Native Rooster (*Gallus gallus domesticus*) Supplemented with Germinated Mung Bean Sprouts and Acidifiers in the Diet

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Table 1. Nutrient compositions of research treatments

Nutrient composition	AIK0 (control)	AIK1	AIK0	AIK1	AIK0	AIK1	AIK0	AIK1
Energy (kcal/kg)	2809	2818	2802	2807	2800	2800	2798	2795
Crude protein (%)	17.20	17.00	17.00	17.00	17.00	17.00	17.00	17.00
Crude fat (%)	3.20	3.10	3.10	3.00	3.10	2.90	3.10	2.90
Crude fiber (%)	4.40	4.40	4.40	4.40	4.30	4.40	4.30	4.40
Ca (%)	0.90	0.90	0.90	0.80	0.80	0.80	0.70	0.70
P (%)	0.50	0.40	0.40	0.40	0.40	0.40	0.40	0.40

AIK0 (control) = 0% mung bean sprout and 0% acidifier, AIK1 = 1% mung bean sprout and 0% acidifier, AIK2 = 1% mung bean sprout and 0.5% acidifier, AIK3 = 1% mung bean sprout and 1% acidifier, AIK4 = 1% mung bean sprout and 1.5% acidifier, AIK5 = 1% mung bean sprout and 2% acidifier.

Table 2. Daily feed consumption and feed conversion of the research data

Treatments	Daily intake (g/head)	FCR
AIK0 (control)	91.75 ± 4.69	1.18 ± 0.06
AIK1	87.56 ± 3.46	1.25 ± 0.13
AIK0	94.11 ± 2.47	1.17 ± 0.11
AIK1	91.49 ± 0.63	1.17 ± 0.13
AIK0	94.14 ± 1.37	1.22 ± 0.09
AIK1	92.45 ± 0.92	1.22 ± 0.03
AIK0	93.00 ± 0.82	1.13 ± 0.10
AIK1	91.94 ± 1.11	1.14 ± 0.06

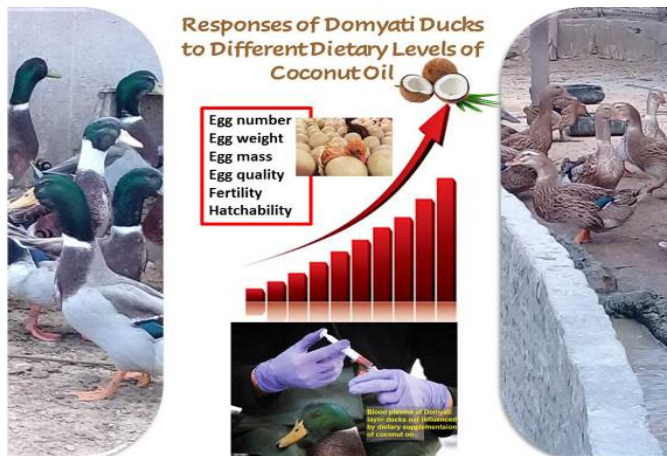
Table 3. Bodyweight and average daily gain of the research data

Treatments	Bodyweight (g)	Average daily gain (g/day)
AIK0 (control)	2,390 ± 228.11	170 ± 60.38
AIK1	2,137 ± 136.52	275 ± 54.79
AIK0	2,425 ± 294.07	240 ± 65.19
AIK1	2,348 ± 138.12	284 ± 115.68
AIK0	2,315 ± 97.34	229 ± 62.12
AIK1	2,281 ± 32.59	229 ± 62.13
AIK0	2,446 ± 198.14	219 ± 26.08
AIK1	2,434 ± 155.28	305 ± 54.93

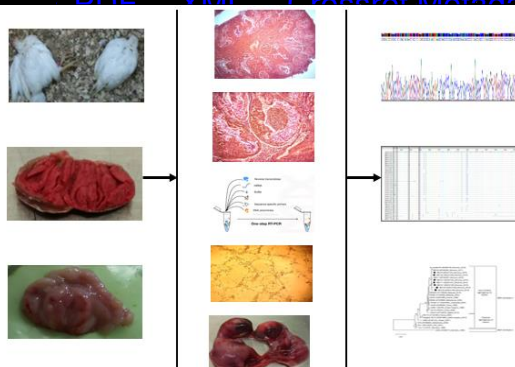
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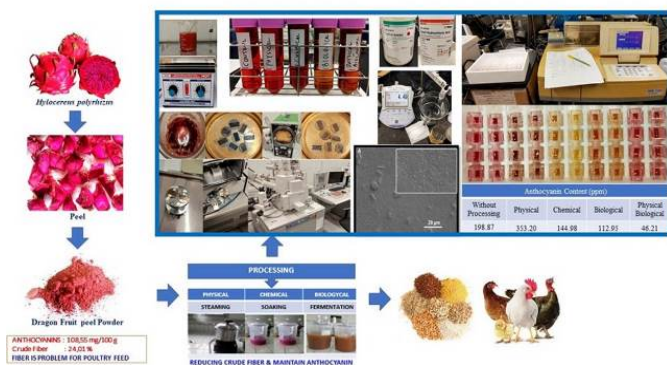
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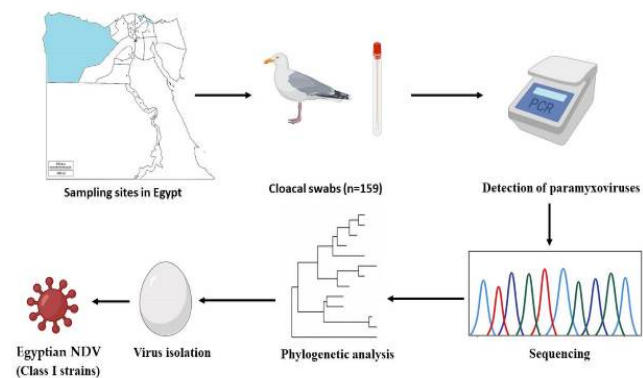
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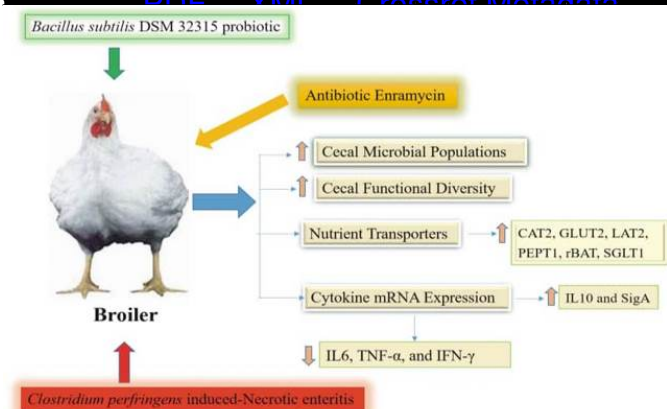
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